

GenCode version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 14:31:01, Search time 40 seconds
(without alignments)
38,467 Million cell updates/sec

Title: US-09-763-848-1

Perfect score: 99

Sequence: 1 PWSSTLGTENLQKPT 16

Scoring table: BLAST2

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9516882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR_76*

2: PIR_2*

3: PIR_1*

4: PIR_4*

Fold. No. is the number of results predicted by chance to have a
score as high as the one observed, assuming random shuffling
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	99	100.0	284	2	S68216	phosphoprotein phosphatase
2	52	52.5	496	2	S42394	G-box-binding protein
3	21	21.5	700	2	S39531	calpain (BC 3.4.22
4	32	32.5	393	2	S77570	transcription factor
5	51	51.5	349	2	S77570	transcription factor
6	51	51.5	700	1	C16H22	calpain (BC 3.4.22
7	49	49.5	805	1	C16H22	calpain (BC 3.4.22
8	49	49.5	1160	2	T23713	hypothetical prote
9	49	49.5	1286	2	T23714	hypothetical prote
10	49	49.5	1286	2	T23714	hypothetical prote
11	48	48.5	601	2	S80150	In heavy chain v r
12	48	48.5	601	2	S80150	probable morphine
13	47.5	48.0	273	2	D71221	Orf 245 protein (1
14	47	47.5	245	2	A60701	phosphatase (BC
15	47	47.5	456	2	T49097	phosphatase (BC
16	47	47.5	566	2	T03855	hypothetical prote
17	47	47.5	703	2	A48764	calpain (BC 3.4.22
18	46	46.5	340	1	C64096	alcohol 1-phosphat
19	46	46.5	340	1	C64096	alcohol 1-phosphat
20	46	46.5	340	1	C64096	alcohol 1-phosphat
21	45	45.5	344	2	T09880	omega-6 desaturase
22	45	45.5	385	2	T09880	omega-6 desaturase
23	45	45.5	385	2	T09880	omega-6 desaturase
24	45	45.5	700	2	S57194	calpain (BC 3.4.22
25	44.5	44.9	177	2	B72560	hypothetical prote
26	44.5	44.9	421	2	A12481	conserved hypothet
27	44.5	44.9	421	2	A12481	conserved hypothet
28	44	44.4	268	2	S06229	chlorophyll a/b-bi
29	44	44.4	401	2	T52250	probable alanine-g

ALIGNMENTS

RESULT 1

S68216

phosphoprotein phosphatase (BC 3.1.3.16) 1 glycogen-binding chain - rat

Alternate names: 33K protein glycogen-binding chain (GTL)

Accession: S68216; S42766; S68723

CDate: 15-Feb-1997 Sequence Revision 13-Mar-1997 West_change 17-Mar-1999

A:Accession: S68216; S42766; S68723

A:Title: Amino acid sequence and expression of the hepatic glycogen-binding (GTL)-

phosphatase. W.J. Morrice and G. Morrice, N. Cohen, P.T.W.

A:Reference number: 568216; MIMD:9008528; PMID:7496521

A:Accession: S68216; S42766; S68723

A:Residues: 1-284 <DOR>

A:Cross-references: GB:S60360; NID:91245930; PID:6145991

A:Keywords: tyrosine kinase

A:Keywords: tyrosine kinase

A:Residues: 21-2413-56;61-98;150-157;161-169;181-199;201-220-228-253;280-284 <DOR>

A:Reference number: 568216; MIMD:9008528; PMID:7496521

A:Accession: S68216; S42766; S68723

A:Title: Purification of the hepatic glycogen-associated form of protein phosphatase

A:Reference number: 568724; MIMD:95237339; PMID:7720853

A:Accession: S68723

A:Residues: 61-76;150-157 <DOR>

A:Experimental source: liver

A:Keywords: glycogen metabolism; phosphoric monoester hydrolase

P: 247;Protein phosphatase 1;glycogen-binding chain status expect

Query Match: 100.0% Score: 99; DB 2: Length: 284;

Matches: 26; Conservative: 0; Identical: 0; Gaps: 0;

DB 269 PWSSTLGTENLQKPT 16

DB 269 PWSSTLGTENLQKPT 284

RESULT 2

S42394

G-box-binding protein - tomato

Accession: S42394

CDate: 15-Feb-1997 Sequence Revision 13-Mar-1999 West_change 21-Jul-2000

A:Accession: S42394

A:Title: Novel conserved sequence motifs in plant G-box binding proteins and implic

A:Reference number: 842394; MIMD:94173701; PMID:8127657

A:Accession: S42394

A:Keywords: Preliminary

A:Residues: 1-405 <DOR>

hypothetical protein W4C9.6a - *Campylobacter jejuni* strain 16374
 C:Species: *Campylobacter jejuni*
 C:Date: 15-Oct-1999 sequence_revision 15-Oct-1999 text_change 15-Oct-1999
 C:Accession: U73714
 C:Map position: 1
 Query Match 49.5%; Score 48; DB 2; Length 601;
 Best Local Similarity 41.7%; Pred. No. 8.6;
 Matches 0; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 submitted to the EMBL Data Library, December 1996
 A:Reference number: Z19787
 A:Status: preliminary; translated from ORF201/203
 A:Molecule type: DNA
 A:Species: *Campylobacter jejuni*
 A:Cross-references: BMJ:283731; FIDN:CA36025.1; GSPDB:GN0019; GSPB:W4C9.6a
 A:Experimental source: clone M4C9
 C:Genetics: W4C9.6a
 A:Map position: 1
 A:Introns: 71/3; 91/3; 114/3; 262/2; 322/2; 374/4; 500/4; 387/2; 445/2; 833/2; 853/3; 893/3
 Query Match 49.5%; Score 49; DB 2; Length 1286;
 Best Local Similarity 42.9%; Pred. No. 26;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 3 WPSLGTATKAG 13
 DB 50 WPSLGTATKAG 60

RESULT 13
 D71221
 probable morphine 6-dehydrogenase - *Pyrococcus horikoshii*
 C:Species: *Pyrococcus horikoshii*
 C:Date: 14-Aug-1998 sequence_revision 14-Aug-1998 text_change 21-Jul-2000
 C:Accession: U73221
 C:Map position: 1
 A:Introns: 10/3; 11/3; 12/3; 13/3; 14/3; 15/3; 16/3; 17/3; 18/3; 19/3; 20/3; 21/3; 22/3; 23/3; 24/3; 25/3; 26/3; 27/3; 28/3; 29/3; 30/3; 31/3; 32/3; 33/3; 34/3; 35/3; 36/3; 37/3; 38/3; 39/3; 40/3; 41/3; 42/3; 43/3; 44/3; 45/3; 46/3; 47/3; 48/3; 49/3; 50/3; 51/3; 52/3; 53/3; 54/3; 55/3; 56/3; 57/3; 58/3; 59/3; 60/3; 61/3; 62/3; 63/3; 64/3; 65/3; 66/3; 67/3; 68/3; 69/3; 70/3; 71/3; 72/3; 73/3; 74/3; 75/3; 76/3; 77/3; 78/3; 79/3; 80/3; 81/3; 82/3; 83/3; 84/3; 85/3; 86/3; 87/3; 88/3; 89/3; 90/3; 91/3; 92/3; 93/3; 94/3; 95/3; 96/3; 97/3; 98/3; 99/3; 100/3; 101/3; 102/3; 103/3; 104/3; 105/3; 106/3; 107/3; 108/3; 109/3; 110/3; 111/3; 112/3; 113/3; 114/3; 115/3; 116/3; 117/3; 118/3; 119/3; 120/3; 121/3; 122/3; 123/3; 124/3; 125/3; 126/3; 127/3; 128/3; 129/3; 130/3; 131/3; 132/3; 133/3; 134/3; 135/3; 136/3; 137/3; 138/3; 139/3; 140/3; 141/3; 142/3; 143/3; 144/3; 145/3; 146/3; 147/3; 148/3; 149/3; 150/3; 151/3; 152/3; 153/3; 154/3; 155/3; 156/3; 157/3; 158/3; 159/3; 160/3; 161/3; 162/3; 163/3; 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1270/3; 1271/3; 1272/3; 1273/3; 1274/3; 1275/3; 1276/3; 1277/3; 1278/3; 1279/3; 1280/3; 1281/3; 1282/3; 1283/3; 1284/3; 1285/3; 1286/3; 1287/3; 1288/3; 1289/3; 1290/3; 1291/3; 1292/3; 1293/3; 1294/3; 1295/3; 1296/3; 1297/3; 1298/3; 1299/3; 1300/3; 1301/3; 1302/3; 1303/3; 1304/3; 1305/3; 1306/3; 1307/3; 1308/3; 1309/3; 1310/3; 1311/3; 1312/3; 1313/3; 1314/3; 1315/3; 1316/3; 1317/3; 1318/3; 1319/3; 1320/3; 1321/3; 1322/3; 1323/3; 1324/3; 1325/3; 1326/3; 1327/3; 1328/3; 1329/3; 1330/3; 1331/3; 1332/3; 1333/3; 1334/3; 1335/3; 1336/3; 1337/3; 1338/3; 1339/3; 1340/3; 1341/3; 1342/3; 1343/3; 1344/3; 1345/3; 1346/3; 1347/3; 1348/3; 1349/3; 1350/3; 1351/3; 1352/3; 1353/3; 1354/3; 1355/3; 1356/3; 1357/3; 1358/3; 1359/3; 1360/3; 1361/3; 1362/3; 1363/3; 1364/3; 1365/3; 1366/3; 1367/3; 1368/3; 1369/3; 1370/3; 1371/3; 1372/3; 1373/3; 1374/3; 1375/3; 1376/3; 1377/3; 1378/3; 1379/3; 1380/3; 1381/3; 1382/3; 1383/3; 1384/3; 1385/3; 1386/3; 1387/3; 1388/3; 1389/3; 1390/3; 1391/3; 1392/3; 1393/3; 1394/3; 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1520/3; 1521/3; 1522/3; 1523/3; 1524/3; 1525/3; 1526/3; 1527/3; 1528/3; 1529/3; 1530/3; 1531/3; 1532/3; 1533/3; 1534/3; 1535/3; 1536/3; 1537/3; 1538/3; 1539/3; 1540/3; 1541/3; 1542/3; 1543/3; 1544/3; 1545/3; 1546/3; 1547/3; 1548/3; 1549/3; 1550/3; 1551/3; 1552/3; 1553/3; 1554/3; 1555/3; 1556/3; 1557/3; 1558/3; 1559/3; 1560/3; 1561/3; 1562/3; 1563/3; 1564/3; 1565/3; 1566/3; 1567/3; 1568/3; 1569/3; 1570/3; 1571/3; 1572/3; 1573/3; 1574/3; 1575/3; 1576/3; 1577/3; 1578/3; 1579/3; 1580/3; 1581/3; 1582/3; 1583

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RESULT 15
A48041
protein kinase (EC 2.7.1.37), cdc2-related CK1 - Leishmania mexicana
C:Accession: A48041.91366
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Author(s): H. H. SMYTH, B. R. TAIT, A. J. BARRY, J. D.
C:J. Biol. Chem. 268, 27044-27052, 1993.
A:Title: A novel Cdc2-related protein kinase from Leishmania mexicana, LmCK1, is post-
A:Reference number: A48041; PMID:94012652; PMID:8407941
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-301 <MDM>
A:Keywords: ATP; phosphotransferase
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:11-19/Region: protein kinase ATP-binding motif
F:34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 47.5% Score 47; DB 1; Length 301;
Best Local Similarity 58.3%; Prod. No. 110
Matches 10; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
CY 1 PERNSTL---QTEKLG 13
DB 251 PERNSTLSTPTKELG 267

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Search completed: October 2, 2003, 14:36:38
Job time : 41 secs

GenCore version 3.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 14:23:45 : search time 22 seconds
(without alignments)
34,201 Million cell updates/sec

Title: US-09-763-848-1

Perfect score: 99

Sequences: 1 P2695107EX/LZPVY 16

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.+

Pred. No. is the number of results predicted by chance to have a
100% identity with the query. The score of the result being printed,
and is derived by analyzing the score above threshold.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	50	52.6	700	1	CM2_MOUSE			006529 Mus musculus
2	52	52.5	700	1	CM2_PAZ			007009 ratius norv
3	51	52.5	349	1	HBA_WHEAT			P33222 triticum ae
4	51	52.5	349	1	HBA_WHEAT			P33222 triticum ae
5	49	49.5	705	1	CM2_CHICK			P00180 homo sapien
6	48	48.5	600	1	CM2_SHITO			007654 sulfolobus
7	48	48.5	600	1	CM2_SHITO			007654 sulfolobus
8	48	48.5	600	1	DN1_SULSU			006469 sulfolobus
9	47	47.5	301	1	CM2_LETME			006509 letismania
10	46	46.5	301	1	CM2_LETME			006509 letismania
11	46	46.5	301	1	CM2_LETME			006509 letismania
12	45	45.5	700	1	FEPA_PATCK			P02773 ratius norv
13	45	45.5	700	1	FEPA_PATCK			P02773 ratius norv
14	44	44.5	268	1	CM2_HUMAN			G03444 homo sapien
15	44	44.5	268	1	CM2_HUMAN			G03444 homo sapien
16	44	44.5	268	1	CM2_HUMAN			G03444 homo sapien
17	43	43.5	120	1	SNH_STRFR			P45799 streptomyce
18	43	43.5	376	1	ALIM_TYEST			P03877 saccharomyce
19	43	43.5	376	1	ALIM_TYEST			P03877 saccharomyce
20	43	43.5	376	1	ALIM_TYEST			P03877 saccharomyce
21	43	43.5	1295	1	BM2_GLABO			045894 streptomyce
22	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
23	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
24	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
25	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
26	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
27	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
28	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
29	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
30	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
31	42	42.5	1295	1	BM2_GLABO			045894 streptomyce
32	41	41.5	870	1	FLB_XILFA			G05671 xyella las
33	41	41.5	885	1	FLB_XANNO			00650 xanthomonas

ALIGNMENTS

RESULTS

ID CM2_MOUSE STANDARD; PER: 700 AA.

AC 006529: 05518: 054843; (last)

DF 15-OCT-2003 (Rev. 40; Last sequence update)

DT 15-SEP-2003 (Rev. 42; Last annotation update)

EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

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EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

EE Calpain 2, large (catalytic) subunit precursor (EC 3.4.22.17)

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: A. 32,724
 REFERENCE/DOCKET NUMBER: G1529
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-5844
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEetical: NO
 US-09-487-942-7

Query Match
 Best Local Similarity 51.5%; Score 51; DB 2; Length 700;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PFWSTGLGKFLGY 15
 DB 52 PAFPSALGKFLGY 66

RESULT 7
 US-09-422-869-23
 Sequence 23 of 23
 GENERAL INFORMATION:
 APPLICANT: POLONSKI, KENNETH S.
 APPLICANT: POLONSKI, KEN
 APPLICANT: POLONSKI, KEN
 APPLICANT: COX, NANCY J.
 APPLICANT: SRENNAN, SEAMUS
 APPLICANT: POLONSKI, KENNETH S.
 APPLICANT: OTANI, CRAIG L.
 APPLICANT: HANIS, CRAIG L.
 APPLICANT: BELL, GRAEME I.
 APPLICANT: BELL, GRAEME I.
 FILE REFERENCE: AR03/307
 CURRENT APPLICATION NUMBER: US/09/422-869
 EARLIER APPLICATION NUMBER: 66/7134,175
 EARLIER FILING DATE: 1999-05-13
 NUMBER OF SEQ ID NOS: 30
 NUMBER OF SEQUENCES: 7
 SEQUENCE LENGTH: 700
 SEQ ID NO: 2, 4
 TYPE: PPT
 TOPOLOGY: linear
 MOLECULE TYPE: Human
 US-09-422-869-23

Query Match
 Best Local Similarity 51.5%; Score 51; DB 3; Length 700;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PFWSTGLGKFLGY 15
 DB 52 PAFPSALGKFLGY 66

RESULT 8
 US-09-083-516-7
 Sequence 7 of 7
 GENERAL INFORMATION:
 APPLICANT: Lin, Lih-Ling
 APPLICANT: Graham, James
 APPLICANT: GRAHAM, JAMES
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
 TITLE OF INVENTION: BINDING
 CORRESPONDENCE ADDRESS:
 ADDRESS: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMMUNICATIONS ROOM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/083-516
 FILING DATE:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 08/487,942

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: A. 32,724
 REFERENCE/DOCKET NUMBER: G1529
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-5844
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEtical: NO
 US-09-763-848-7

Query Match
 Best Local Similarity 60.0%; Pred. No. 8;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PFWSTGLGKFLGY 15
 DB 52 PAFPSALGKFLGY 66

RESULT 9
 US-09-083-516-7
 Sequence 7 of 7
 GENERAL INFORMATION:
 APPLICANT: Lin, Lih-Ling
 APPLICANT: Graham, James
 APPLICANT: GRAHAM, JAMES
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
 TITLE OF INVENTION: BINDING
 CORRESPONDENCE ADDRESS:
 ADDRESS: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMMUNICATIONS ROOM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/763-848-7
 FILING DATE:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 08/487,942

```

1 FILING DATE:
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Brown, Scott A.
4 REFERENCE/DOCKET NUMBER: G15258
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (617) 438-8224
7 INFORMATION FOR SEQ ID NO: 7:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 700 amino acids
10 STRANDNESS: single
11 TOPOLOGY: linear
12 MODIFICATION: none
13 NOVELTY: Protein
14 BIOCHEMICAL: NO
15 US-09-083-516-7
16
17 Query Match 51.5%; Score 51; DB 4; Length 700;
18 Best Local Similarity 60.0%; Pred. No. 8;
19 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
20
21 QY 1 EPOSAFGEKGGPT 15
22 DB 52 PAISAFGEKGGPT 66
23
24 RESULT 9
25 US-09-593-465-19
26 Sequence 12, Application US/08953155A
27 Patent No. 6123523
28 GENERAL INFORMATION:
29 APPLICANT: Unger, Evan C.
30 APPLICANT: No. Unger
31 TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use
32 CURRENT APPLICATION NUMBER: US/08/993,465A
33 CURRENT FILING DATE: 1997-12-18
34 NUMBER OF SEQ ID NOS: 40
35 SUMMARY OF SEQ ID NOS: 2.1
36 SEQ ID NO 12
37 LENGTH: 19
38 SEQ ID NO 19
39 ORGANISM: Artificial Sequence
40 FEATURE:
41 OTHER INFORMATION: Description of Artificial Sequence: No. 6123923al Sequence
42 US-09-593-403-12
43
44 Query Match 48.5%; Score 48; DB 3; Length 19;
45 Best Local Similarity 51.5%; Pred. No. 0.51;
46 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
47
48 QY 4 PSTLGEKGGPT 16
49 DB 3 PSYTFDGGPT 15
50
51 RESULT 10
52 US-09-540-448-12
53 Sequence 12, Application US/09510448
54 Patent No. 6123523
55 GENERAL INFORMATION:
56 APPLICANT: Unger, Evan C.
57 APPLICANT: No. Unger
58 TITLE OF INVENTION: Unsaturated Lipids and Uses For The Same
59 CURRENT APPLICATION NUMBER: US/09/540,448
60 CURRENT FILING DATE: 2000-03-31
61 PRIOR FILING DATE: 1997-09-08
62 NUMBER OF SEQ ID NOS: 37
63 SUMMARY OF SEQ ID NOS: 2.1
64 SEQ ID NO 12
65 LENGTH: 19
66 SEQ ID NO 19
67 ORGANISM: Artificial Sequence
68 FEATURE:
69 OTHER INFORMATION: Description of Artificial Sequence: No. 6521211al Sequence
70 US-09-547-640-10
71
72 Query Match 48.5%; Score 48; DB 4; Length 19;
73 Best Local Similarity 51.5%; Pred. No. 0.51;
74 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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76 QY 4 PSTLGEKGGPT 16
77 DB 3 PSYTFDGGPT 15
78
79 RESULT 12
80 US-08-925-847-12
81 Sequence 12, Application US/08929847
82 Patent No. 6123523
83 GENERAL INFORMATION:
84 APPLICANT: Unger, Evan C.
85 APPLICANT: No. Unger
86 TITLE OF INVENTION: Chemical Inactivation Of Gaseous Precursor Filled Compositions
87 CURRENT APPLICATION NUMBER: US/08/929,847
88 CURRENT FILING DATE: 1997-09-15
89 PRIOR FILING DATE: 1997-09-15
90 NUMBER OF SEQ ID NOS: 35
91 SUMMARY OF SEQ ID NOS: 3.1
92 SEQ ID NO 12
93 LENGTH: 19
94 SEQ ID NO 19
95 ORGANISM: Artificial Sequence
96 FEATURE:
97 OTHER INFORMATION: Description of Artificial Sequence: No. 6521211al Sequence
98 US-09-547-640-10

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: FEATURE:
: OTHER INFORMATION: Completely synthetic sequence
US-08-929-447-12
: SEQUENCE 13, Application US/0893165A
: Score 48; DB 4; Length 19;
Query Match 61.5%; Pred. No. 0.51;
Best Local Similarity 61.5%; Mismatches 4; Indels 0; Gaps 0;
Matches 8; Conservative 1;
QY 4 PSYLOGEKGPT 16
DB 3 PSYRINOGAGPT 15

RESULT 13
US-08-923-640-11
: SEQUENCE 13, Application US/0893165A
: Patent No. 6123211
: GENERAL INFORMATION:
: APPLICANT: Unger, Evan C
: APPLICANT: US, GSK
: APPLICANT: Wu, Guanli
: TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use
: CURRENT APPLICATION NUMBER: US/08/993.165A
: CURRENT FILING DATE: 1997-12-18
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 13
: LENGTH: 21
: SEQ ID NO 11
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: No. 6123923al Sequence
US-09-763-648-1
: SEQUENCE 13, Application US/09540448
: Score 48; DB 3; Length 21;
Query Match 61.5%; Pred. No. 0.56;
Best Local Similarity 61.5%; Mismatches 4; Indels 0; Gaps 0;
Matches 8; Conservative 1;
QY 4 PSYLOGEKGPT 16
DB 5 PSYRINOGAGPT 17

RESULT 14
US-09-540-448-13
: SEQUENCE 13, Application US/09540448
: Patent No. 6123923
: GENERAL INFORMATION:
: APPLICANT: Unger, Evan C.
: TITLE OF INVENTION: Charged Lipids and Uses For The Same
: CURRENT APPLICATION NUMBER: US/09/540.448
: CURRENT FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 13
: LENGTH: 21
: ORGANISM: Artificial Sequence
: TYPE: PPT
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: No. 6403056al Sequence
US-09-540-448-13
: SEQUENCE 13, Application US/09540448
: Score 48; DB 4; Length 21;
Query Match 61.5%; Pred. No. 0.56;
Best Local Similarity 61.5%; Mismatches 4; Indels 0; Gaps 0;
Matches 8; Conservative 1;
QY 4 PSYLOGEKGPT 16
DB 5 PSYRINOGAGPT 17

RESULT 15
US-09-243-640-11
: SEQUENCE 13, Application US/09243640
: Patent No. 6521211
: GENERAL INFORMATION:
: APPLICANT: Unger, Evan C
: APPLICANT: US, GSK
: APPLICANT: Wu, Guanli
: TITLE OF INVENTION: No. 6521211al Methods Of Imaging And Treatment With Targeted Contrast Agents And Methods
: FILE REFERENCE: JUP-3463
: CURRENT APPLICATION NUMBER: US/09/213.640
: CURRENT FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: 05/66.032
: PRIOR FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: 05/640.464
: PRIOR FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: 05/497.684
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 05/218.660
: PRIOR FILING DATE: 1998-02-05
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 11
: LENGTH: 21
: SEQ ID NO 11
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: No. 6521211al Sequence
US-09-243-640-11
: SEQUENCE 13, Application US/09243640
: Score 48; DB 4; Length 21;
Query Match 61.5%; Pred. No. 0.56;
Best Local Similarity 61.5%; Mismatches 4; Indels 0; Gaps 0;
Matches 8; Conservative 1;
QY 4 PSYLOGEKGPT 16
DB 5 PSYRINOGAGPT 17

Search completed: October 2, 2003, 14:37:14
Job time : 30 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

ON protein - protein search, using sw model

Run on: October 2, 2003, 14:36:01 ; Search time 66 Seconds
(without alignments)
36.355 Million cell updates/sec

Title: US-09-763-848-1

Perfect score: 99

Sequence: 1 PFMSTAYKLEKPTV 16

Scoring table: BLOSUM62

Gapop 10.0 ; Gapex: 0.5

Searched: 597654 seqs, 15821981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

- 1: /cgn2.6/pdata/2/pubpa/US07_PUBCOMB pep.*
- 2: /cgn2.6/pdata/2/pubpa/US07_NEM_PUB pep.*
- 3: /cgn2.6/pdata/2/pubpa/US06_PUBCOMB pep.*
- 4: /cgn2.6/pdata/2/pubpa/US06_PUBCOMB pep.*
- 5: /cgn2.6/pdata/2/pubpa/US07_NEM_PUB pep.*
- 6: /cgn2.6/pdata/2/pubpa/US07_PUBCOMB pep.*
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- 12: /cgn2.6/pdata/2/pubpa/US09_NEM_PUB pep.*
- 13: /cgn2.6/pdata/2/pubpa/US10_PUBCOMB pep.*
- 14: /cgn2.6/pdata/2/pubpa/US10_PUBCOMB pep.*
- 15: /cgn2.6/pdata/2/pubpa/US10C_PUBCOMB pep.*
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	99	100.0	285	9	US-09-737-149-42	Sequence 42, Appl
3	99	100.0	285	9	US-09-737-149-12	Sequence 12, Appl
4	51	51.5	700	0	US-09-840-707A-9	Sequence 9, Appl
5	51	51.5	700	0	US-09-768-877-23	Sequence 23, Appl
6	51	51.5	700	11	US-10-884-555F-9	Sequence 9, Appl
7	51	51.5	700	11	US-10-884-555F-9	Sequence 11, Appl
8	51	51.5	700	15	US-10-116-519-12	Sequence 12, Appl
9	51	51.5	700	15	US-10-046-808-12	Sequence 12, Appl
10	48	48.5	13	15	US-10-246-984-13	Sequence 13, Appl
11	48	48.5	223	15	US-10-246-984-13	Sequence 13, Appl
12	48	48.5	253	15	US-10-239-358A-24	Sequence 24, Appl
13	48	48.5	450	15	US-10-062-848-9	Sequence 9, Appl
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15	48	48.5	466	14	US-10-083-453A-13	Sequence 13, Appl

16	47	47.5	647	15	US-10-116-519-10	Sequence 10, Appl
17	47	47.5	703	10	US-09-788-877-27	Sequence 27, Appl
18	47	47.5	703	10	US-09-788-877-27	Sequence 27, Appl
19	47	47.5	703	10	US-10-156-791-150667	Sequence 150667, Appl
20	45	45.5	535	10	US-09-837-751-4	Sequence 4, Appl
21	45	45.5	748	12	US-10-021-660-81	Sequence 81, Appl
22	44	44.4	253	15	US-10-021-660-81	Sequence 81, Appl
23	44	44.4	253	15	US-10-287-401-30	Sequence 30, Appl
24	43	43.4	111	9	US-09-898-898-7	Sequence 7, Appl
25	43	43.4	253	11	US-09-880-748-1835	Sequence 1835, Appl
26	42	42.4	133	12	US-09-880-748-1835	Sequence 1835, Appl
27	42	42.4	133	12	US-09-903-190-103	Sequence 103, Appl
28	42	42.4	343	9	US-09-794-960-4	Sequence 4, Appl
29	42	42.4	383	9	US-09-852-392-4	Sequence 4, Appl
30	42	42.4	383	9	US-09-852-392-4	Sequence 4, Appl
31	42	42.4	399	15	US-10-287-401-4	Sequence 4, Appl
32	42	42.4	434	12	US-10-097-111-290	Sequence 290, Appl
33	42	42.4	434	12	US-10-097-111-290	Sequence 290, Appl
34	42	42.4	434	12	US-09-910-186A-6	Sequence 6, Appl
35	42	42.4	434	12	US-09-910-186A-6	Sequence 6, Appl
36	42	42.4	437	11	US-09-910-186A-7	Sequence 7, Appl
37	42	42.4	437	11	US-09-910-186A-7	Sequence 7, Appl
38	42	42.4	714	10	US-09-768-877-22	Sequence 22, Appl
39	42	42.4	714	15	US-10-116-519-6	Sequence 6, Appl
40	42	42.4	722	15	US-09-768-877-22	Sequence 22, Appl
41	42	42.4	722	15	US-09-926-348A-5	Sequence 5, Appl
42	41.9	41.9	152	9	US-09-815-242-13962	Sequence 13962, A
43	41	41.4	1246	9	US-09-741-659-349	Sequence 349, Appl
44	41	41.4	1246	9	US-09-741-659-349	Sequence 349, Appl
45	41	41.4	1247	9	US-09-815-242-13841	Sequence 13841, A

ALIGNMENTS

RESUME 1
Sequence 43, Application US/09737149
Patent No. US200200776681
APPLICANT: Spadaro, Steven K
APPLICANT: Quinn, Kerry E
APPLICANT: Shlensky, Richard A
APPLICANT: Shlensky, Richard A
APPLICANT: Stryker, Kimberly A
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/09737149
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR FILING DATE: 2000-05-07
PRIOR APPLICATION NUMBER: 60/175,929
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQUENCE LENGTH: 282
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Consensus Sequence
NAME/KEY: VARIANT
LOCATION: (1)..(242)

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 2, 2003, 14:23:05 (search time 82 seconds)

Title: US-09-763-848-1

Perfect score: 99

Sequence: 1 FFWSTGLATFLDY 16

Scoring table: BLOSUM62 Gap: 10.0, Gap: 0.5

Searched: 110763 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Width: 08

Maximum Match: 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	a	Score	Match	Length	DB ID	Description
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3	99	100.0	285	22	AA35503	Human protein phosphatase-1 (PP-1).
4	90	90.9	16	21	AA70664	C-terminal peptide
5	52	52.5	700	22	AAH6130	Rat calpain 80kDa
6	52	52.5	700	22	AAH6130	Rat calpain 80kDa
7	51	51.5	700	28	AAH1932	Human calpain
8	51	51.5	700	21	AAH1737	Human calpain
9	51	51.5	700	22	AAH6128	Human calpain 80kDa

10	51	51.5	700	23	AA25059	Human calpain prot
11	50	50.5	447	23	AAH9720	Marine calpain2 prot
12	50	50.5	462	23	AAH9720	Marine calpain2 prot
13	50	50.5	462	23	AAH9720	Marine calpain2 prot
14	50	50.5	720	23	AAH9721	Marine calpain2 prot
15	48.5	49.0	82	23	AAH10799	Human ORF protein
16	48	48.5	19	33	AAH5549	Targeting ligand
17	48	48.5	19	33	AAH5549	Targeting ligand
18	48	48.5	19	33	AAH5549	Targeting ligand
19	48	48.5	21	18	AAH5498	Targeting ligand
20	48	48.5	21	18	AAH5498	Targeting ligand
21	48	48.5	21	18	AAH5498	Targeting ligand
22	48	48.5	26	12	AAH15276	Glycoprotein Orib
23	48	48.5	27	12	AAH15276	Glycoprotein Orib
24	48	48.5	27	12	AAH15276	Glycoprotein Orib
25	48	48.5	219	15	AAH56235	Anti-thrombic fusi
26	48	48.5	219	15	AAH56235	Anti-thrombic fusi
27	48	48.5	233	15	AAH56236	Anti-thrombic fusi
28	48	48.5	233	15	AAH56236	Anti-thrombic fusi
29	48	48.5	233	15	AAH56236	Anti-thrombic fusi
30	48	48.5	443	21	AAH20312	166-116/112-65/11-
31	48	48.5	443	21	AAH20312	166-116/112-65/11-
32	48	48.5	443	21	AAH20312	166-116/112-65/11-
33	47	47.5	300	22	AAH95363	Taleomycos thermo
34	47	47.5	392	21	AAH70999	Taleomycos thermo
35	47	47.5	392	21	AAH70999	Taleomycos thermo
36	47	47.5	429	21	AAH7098	Taleomycos thermo
37	47	47.5	429	21	AAH7098	Taleomycos thermo
38	47	47.5	703	18	AAH1564	Human calpain. Ho
39	47	47.5	703	18	AAH1564	Human calpain. Ho
40	47	47.5	703	23	AAH72884	Human calpain. Ho
41	47	47.5	712	18	AAH1565	Human calpain. Ho
42	47	47.5	712	18	AAH1565	Human calpain. Ho
43	46	46.5	467	23	AAH5059	Human calpain prot
44	46	46.5	467	23	AAH5059	Human calpain prot
45	46	46.5	467	23	AAH70268	Human calpain-like

ALIGNMENTS

RESULT 1
 AAH14236
 AAH14236 standard; Protein: 284 AA.

AAH14236:

AC AC 07-MAR-2002 (first entry)

DE Human protein phosphatase-1 (PP-1).

Human: protein phosphatase-1; pp1; gene therapy; tauquilliser; amnesia;
 artter; sclerotic; atherosclerosis; anxiety; anemia; hepatitis; catarrh;
 myographic lateral sclerosis; menocarcinoma; cerebral palsy; scrotales;
 neurological disorder; epilepsy; neoplasm; Alzheimer's disease; dementia;
 thyroiditis; dermatitis; diabetic mellitus; rheumatoid arthritis; stroke;
 granulomatous disease; hemolytic anaemia; chrom's disease; cancer; SCID;
 developmental disorder; cell proliferative disorder; Addison's disease;
 systemic lupus erythematosus; Parkinson's disease; myofibrillar; AIDS;
 leukemia; antiinflammatory; cirrhosis; muscular dystrophy; allergy.

CS Homo sapiens.

XX XN W0300181500-A2.

XX PD 01-XIV-2001.

XX XN 19-APR-2001; 2001W05-12902.

XX XN 20-APR-2000; 2000G5-190010P.

XX XN 05-MAR-2000; 2000G5-202340P.

KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

OS Homo sapiens.

XX W0200159253-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001PC-US-0836.

XX 30-MAY-2000; 2000US-204132P.

XX 29-AUG-2000; 2000US-228716P.

XX (CUBA-) CUBAGEN CORE.

XX Shimkuts RA, Leach MD.

XX WPI: 2002-106308/14.

XX N-PGDP; ABM28554.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders

XX Disclosure: SEQ ID 21580; 1037pp; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-1431 (see Table 1
 CC in the specification). ABM15762 to ABM27252 encode the human ORFX
 CC proteins given in ABM00010 to ABM1500. ORFX proteins are useful for
 CC diagnosing, preventing and treating cardiovascular disease, neurodegenerative
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences in genes encoding ORFX proteins are useful for the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, hemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC dysfunction, autoimmune disorders, autoimmune diseases, rheumatoid
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, psoriasis, Crohn's disease, ulcerative
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC for preventing and treating reperfusion injury, for preventing and
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC reperfusion damage.
 CC A genome database for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from MPO
 CC at ftp.mipo.it/pub/published_get_sequences.

XX Sequence 82 AA;

Query Match 45 04; Score 48.5; DB 23; Length 82;
 Query Similarity 60.0; Positives 1;
 Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Db 32 PDPSPG-REKLEP 46

Search completed: October 2, 2003, 14:33:40

Job time : 83 secs